



SEQUENCE LISTING

<110> Sukhaphinda, Kitisri
Hasler, James M
Petell, James K
Strickland, James A
Folkerts, Otto

<120> ANTIBODY-MEDIATED DOWN-REGULATION OF PLANT PROTEINS

<130> 50447

<140> US 09/358,321

<141> 1999-07-21

<150> US 60/093,587

<151> 1998-07-21

<160> 56

<170> PatentIn Ver. 2.0

<210> 1

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:5' primer

<220>

<221> unsure

<222> (12)

<223> n can be a,t,g, or c in this degenerate primer

<400> 1

gargaraaym gncaygg

17

<210> 2

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3' primer

<220>

<221> unsure

<222> (7)

<223> n can be a,t,g, or c in this degenerate primer

<400> 2

ytcrtgncy ttytcrtc

18

<210> 3

<211> 276

<212> DNA

<213> Zea mays

<220>
 <221> CDS
 <222> (1)..(276)

<400> 3

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1 5 10 15	
ggg agg gtg gat atg agg cag att gag aag aca att cag tat ctt att	96
Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile	
20 25 30	
ggc tct gga atg gat cct agg act gag aat aat cct tat ctt ggt ttc	144
Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe	
35 40 45	
atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac ggg aac	192
Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn	
50 55 60	
act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca caa atc	240
Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile	
65 70 75 80	
tgc ggc atc atc gcc tca gat gag aag cga cat gaa	276
Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu	
85 90	

<210> 4
 <211> 92
 <212> PRT
 <213> Zea mays

<400> 4

Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr	
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Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile	
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Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe	
35 40 45	
Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn	
50 55 60	
Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile	
65 70 75 80	
Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu	
85 90	

<210> 5
 <211> 1621
 <212> DNA
 <213> Zea mays

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<220>  
<221> mat_peptide  
<222> (239)..(1324)
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155 160 165 170	
ctt att ggc tct gga atg gat cct agg act gag aat aat cct tat ctt	796
Leu Ile Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu	
175 180 185	
ggt ttc atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac	844
Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His	
190 195 200	
ggg aac act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca	892
Gly Asn Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala	
205 210 215	
caa atc tgc ggc atc atc gcc tca gat gag aag cga cat gaa act gcg	940
Gln Ile Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala	
220 225 230	
tac acc aag atc gtg gag aag ctg ttt gag atc gac cct gat ggt acc	988
Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr	
235 240 245 250	
gtg gtc gct ctg gct gac atg atg agg aag aag atc tca atg cct gcc	1036
Val Val Ala Leu Ala Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala	
255 260 265	
cac ctg atg ttt gac ggg cag gac gac aag ctg ttc gag cac ttc tcc	1084
His Leu Met Phe Asp Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser	
270 275 280	
atg gtc gcg cag agg ctt ggc gtt tac acc gcc agg gac tac gcc gac	1132
Met Val Ala Gln Arg Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp	
285 290 295	
atc ctc gag ttc ctc gtc gac agg tgg aag gtg gcg agc ctg act ggt	1180
Ile Leu Glu Phe Leu Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly	
300 305 310	
ctg tcg ggt gaa ggg aac aag gcg cag gac tac ctt tgc acc ctt gct	1228
Leu Ser Gly Glu Gly Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala	
315 320 325 330	
tca aga atc agg agg ctg gag gag agg gcc cag agc aga gcc aag aaa	1276
Ser Arg Ile Arg Arg Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys	
335 340 345	
gcc ggc acg ctg cct ttc agc tgg gta tac ggt agg gac gtc caa ctg	1324
Ala Gly Thr Leu Pro Phe Ser Trp Val Tyr Gly Arg Asp Val Gln Leu	
350 355 360	
tgagatcgga aacctgctgc ggactgctta gacaagacct gctgtgtctg cgttacatag	1384
gtctccaggt tttgatcaaa tgggtcccggtg tcgtcttata gagcgatagg agaacgtgtt	1444
ggctctgtggt gtagctttgt ttttatttttg tattttttctg ctttgatgta caacctgtgg	1504
ccgcatgaac tggggcggtgg agatgggagc gaccatgccg tactttgtct gtcgctggcg	1564
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<210> 6
 <211> 393
 <212> PRT
 <213> Zea mays

<400> 6

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Ala	Ala	Arg	Arg	Arg	Arg	Arg	Ser	Ser	Gly	Arg	Phe	Val	Ala	Val	Ala
-15					-10				-5				-1		1
Ser	Met	Thr	Ser	Ala	Val	Ser	Thr	Lys	Val	Glu	Asn	Lys	Lys	Pro	Phe
			5					10					15		
Ala	Pro	Pro	Arg	Glu	Val	His	Val	Gln	Val	Thr	His	Ser	Met	Pro	Pro
		20					25					30			
His	Lys	Ile	Glu	Ile	Phe	Lys	Ser	Leu	Asp	Asp	Trp	Ala	Arg	Asp	Asn
35						40					45				
Ile	Leu	Thr	His	Leu	Lys	Pro	Val	Glu	Lys	Cys	Trp	Gln	Pro	Gln	Asp
50					55					60					65
Phe	Leu	Pro	Asp	Pro	Ala	Ser	Glu	Gly	Phe	His	Asp	Glu	Val	Lys	Glu
				70					75					80	
Leu	Arg	Glu	Arg	Ala	Lys	Glu	Ile	Pro	Asp	Asp	Tyr	Phe	Val	Cys	Leu
			85					90					95		
Val	Gly	Asp	Met	Ile	Thr	Glu	Glu	Ala	Leu	Pro	Thr	Tyr	Gln	Thr	Met
		100					105						110		
Leu	Asn	Thr	Leu	Asp	Gly	Val	Arg	Asp	Glu	Thr	Gly	Ala	Ser	Pro	Thr
115						120					125				
Ala	Trp	Ala	Val	Trp	Thr	Arg	Ala	Trp	Thr	Ala	Glu	Glu	Asn	Arg	His
130					135					140					145
Gly	Asp	Leu	Leu	Asn	Lys	Tyr	Met	Tyr	Leu	Thr	Gly	Arg	Val	Asp	Met
				150					155					160	
Arg	Gln	Ile	Glu	Lys	Thr	Ile	Gln	Tyr	Leu	Ile	Gly	Ser	Gly	Met	Asp
			165					170					175		
Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr	Leu	Gly	Phe	Ile	Tyr	Thr	Ser	Phe
		180					185					190			
Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser	His	Gly	Asn	Thr	Ala	Arg	His	Ala
195						200					205				
Lys	Asp	Phe	Gly	Asp	Leu	Lys	Leu	Ala	Gln	Ile	Cys	Gly	Ile	Ile	Ala
210					215					220					225
Ser	Asp	Glu	Lys	Arg	His	Glu	Thr	Ala	Tyr	Thr	Lys	Ile	Val	Glu	Lys
				230					235					240	
Leu	Phe	Glu	Ile	Asp	Pro	Asp	Gly	Thr	Val	Val	Ala	Leu	Ala	Asp	Met
			245					250					255		

Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp Gly Gln
260 265 270

Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg Leu Gly
275 280 285

Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Asp
290 295 300 305

Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys
310 315 320

Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg Leu Glu
325 330 335

Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro Phe Ser
340 345 350

Trp Val Tyr Gly Arg Asp Val Gln Leu
355 360

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 7
atggctagcc tccgcctcaa cgacgtcgcg 30

<210> 8
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 8
aaagctagct catcacagtt ggacgtccct accgta 36

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 9
accatggcta gcatgacgtc cgccgtctcc 30

<210> 10
<211> 30

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 10
 gatgatgcta gctcacagtt ggacgtccct 30

<210> 11
 <211> 1107
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (4)..(1092)

<400> 11
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 1 5 10 15

aag cca ttt gct cct cca agg gag gta cat gtc cag gtt aca cat tca 96
 Lys Pro Phe Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser
 20 25 30

atg cca cct cac aag att gaa att ttc aag tcg ctt gat gat tgg gct 144
 Met Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala
 35 40 45

aga gat aat atc ttg acg cat ctc aag cca gtc gag aag tgt tgg cag 192
 Arg Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln
 50 55 60

cca cag gat ttc ctc ccg gac cca gca tct gaa gga ttt cat gat gaa 240
 Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu
 65 70 75

gtt aag gag ctc aga gaa cgt gcc aag gaa atc cct gat gat tat ttt 288
 Val Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe
 80 85 90 95

gtt tgt ttg gtg gga gac atg att acc gag gaa gct cta cca aca tac 336
 Val Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr
 100 105 110

cag act atg ctt aac acc ctc gac ggt gtc aga gat gag aca ggt gca 384
 Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala
 115 120 125

agc ccc act gcc tgg gct gtt tgg acg agg gca tgg act gct gag gag 432
 Ser Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu
 130 135 140

aac agg cat ggt gat ctg ctc aac aag tat atg tac ctc act ggg agg 480
 Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg
 145 150 155

gtg gat atg agg cag att gag aag aca att cag tat ctt att ggc tct 528

Val 160	Asp	Met	Arg	Gln	Ile 165	Glu	Lys	Thr	Ile	Gln 170	Tyr	Leu	Ile	Gly	Ser 175	
gga Gly	atg Met	gat Asp	cct Pro	agg Arg	act Thr	gag Glu	aat Asn	aat Asn	cct Pro	tat Tyr	ctt Leu	ggt Gly	ttc Phe	atc Ile	tac Tyr	576
acc Thr	tcc Ser	ttc Phe	caa Gln	gag Glu	cgg Arg	gcg Ala	acc Thr	ttc Phe	atc Ile	tca Ser	cac His	ggg Gly	aac Asn	act Thr	gct Ala	624
cgt Arg	cac His	gcc Ala	aag Lys	gac Asp	ttt Phe	ggc Gly	gac Asp	tta Leu	aag Lys	ctt Leu	gca Ala	caa Gln	atc Ile	tgc Cys	ggc Gly	672
atc Ile	atc Ile	gcc Ala	tca Ser	gat Asp	gag Glu	aag Lys	cga Arg	cat His	gaa Glu	act Thr	gcg Ala	tac Tyr	acc Thr	aag Lys	atc Ile	720
gtg Val	gag Glu	aag Lys	ctg Leu	ttt Phe	gag Glu	atc Ile	gac Asp	cct Pro	gat Asp	ggt Gly	acc Thr	gtg Val	gtc Val	gct Ala	ctg Leu	768
gct Ala	gac Asp	atg Met	atg Met	agg Arg	aag Lys	aag Lys	atc Ile	tca Ser	atg Met	cct Pro	gcc Ala	cac His	ctg Leu	atg Met	ttt Phe	816
gac Asp	ggg Gly	cag Gln	gac Asp	gac Asp	aag Lys	ctg Leu	ttc Phe	gag Glu	cac His	ttc Phe	tcc Ser	atg Met	gtc Val	gcg Ala	cag Gln	864
agg Arg	ctt Leu	ggc Gly	gtt Val	tac Tyr	acc Thr	gcc Ala	agg Arg	gac Asp	tac Tyr	gcc Ala	gac Asp	atc Ile	ctc Leu	gag Glu	ttc Phe	912
ctc Leu	gtc Val	gac Asp	agg Arg	tgg Trp	aag Lys	gtg Val	gcg Ala	agc Ser	ctg Leu	act Thr	ggt Gly	ctg Leu	tgc Ser	ggt Gly	gaa Glu	960
ggg Gly	aac Asn	aag Lys	gcg Ala	cag Gln	gac Asp	tac Tyr	ctt Leu	tgc Cys	acc Thr	ctt Leu	gct Ala	tca Ser	aga Arg	atc Ile	agg Arg	1008
agg Arg	ctg Leu	gag Glu	gag Glu	agg Arg	gcc Ala	cag Gln	agc Ser	aga Arg	gcc Ala	aag Lys	aaa Lys	gcc Ala	ggc Gly	acg Thr	ctg Leu	1056
cct Pro	ttc Phe	agc Ser	tgg Trp	gta Val	tac Tyr	ggt Gly	agg Arg	gac Asp	gtc Val	caa Gln	ctg Leu	tgagctagca	tcac			1107

<210> 12
 <211> 363
 <212> PRT
 <213> Zea mays

<400> 12
 Met Ala Thr Met Thr Ser Ala Val Ser Thr Lys Val Glu Asn Lys Lys
 1 5 10 15

Pro Phe Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser Met
 20 25 30
 Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg
 35 40 45
 Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro
 50 55 60
 Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu Val
 65 70 75 80
 Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val
 85 90 95
 Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln
 100 105 110
 Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser
 115 120 125
 Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn
 130 135 140
 Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg Val
 145 150 155 160
 Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly
 165 170 175
 Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr
 180 185 190
 Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg
 195 200 205
 His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile Cys Gly Ile
 210 215 220
 Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val
 225 230 235 240
 Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Val Ala Leu Ala
 245 250 255
 Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp
 260 265 270
 Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg
 275 280 285
 Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu
 290 295 300
 Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu Gly
 305 310 315 320
 Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg
 325 330 335
 Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro

<220>
 <223> Description of Artificial Sequence:primer

 <400> 17
 aaagctagcc tsctgcygyt ctkkttwycw ggtryc 36

 <210> 18
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 18
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 <210> 19
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 19
 tttgctagct tactaacact cattcctgtt gaagctct 38

 <210> 20
 <211> 102
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 20
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 cattctgcct ttgcggcgggt tgtgatgacc ccaaaccac tc 102

 <210> 21
 <211> 738
 <212> DNA
 <213> mouse

 <220>
 <221> unsure
 <222> (16)..(21)
 <223> not known

 <220>
 <221> unsure
 <222> (26)
 <223> not known

 <220>

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<220>
<221> CDS
<222> (37) .. (693)
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				1				5		
aac cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct	102									
Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser										
	10			15				20		
tgc aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta	150									
Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu										
	25			30				35		
cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac	198									
His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr										
	40			45				50		
aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt	246									
Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser										
	55			60				65		70
gga tca ggg aca gat ttc aca ctc aag atc aac aga gtg gag gct gag	294									
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Asn Arg Val Glu Ala Glu										
	75			80				85		
gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg	342									
Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr										
	90			95				100		
ttc gga ggg ggg acc aag ctg gaa ata aaa cgg gct gat gct gca cca	390									
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro										
	105			110				115		
act gta tcc atc ttc cca cca tcc agt gag cag tta aca tct gga ggt	438									
Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly										
	120			125				130		
gcc tca gtc gtg tgc ttc ttg aac aac ttc tac ccc aaa gac atc aat	486									
Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn										
	135			140				145		150
gtc aag tgg aag att gat ggc agt gaa cga caa aat ggc gtc ctg aac	534									
Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn										
	155			160				165		
agt tgg act gat cag gac acc aaa gac agc acc tac agc atg agc agc	582									
Ser Trp Thr Asp Gln Asp Thr Lys Asp Ser Thr Tyr Ser Met Ser Ser										
	170			175				180		
acc ctc acg ttg acc aag gac gag tat gaa cga cat aac agc tat acc	630									
Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr										
	185			190				195		

tgt gag gcc act cac aag aca tca act tca ccc att gtc aag agc ttc	678
Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe	
200 205 210	

aac agg aat gag tgt tagtaagcta gcacgcccga tgggtgggacg gtatgaataa	733
Asn Arg Asn Glu Cys	
215	

tccgg	738
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<210> 22
 <211> 336
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (1)..(336)

<400> 22	
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1 5 10 15	

gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt	96
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser	
20 25 30	

aat gga atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct	144
Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
35 40 45	

cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca	192
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro	
50 55 60	

gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	
65 70 75 80	

aac aga gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt	288
Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser	
85 90 95	

aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa	336
Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
100 105 110	

<210> 23
 <211> 108
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

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gcgcattctg cctttgcggc ggttcaactg cagcagtctg gggctgag

108

<210> 24
<211> 882
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (25)..(837)

<220>
<221> mat_peptide
<222> (79)..(837)

<400> 24
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Met Thr Ile Leu Cys Trp Leu Ala Leu
-15 -10

ctg tca act ctg act gcc gtc aac act gcg gtt gtg atg acc cca aac 99
Leu Ser Thr Leu Thr Ala Val Asn Thr Ala Val Val Met Thr Pro Asn
-5 -1 1 5

cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc 147
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
10 15 20

aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat 195
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His
25 30 35

tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa 243
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
40 45 50 55

gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 291
Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
60 65 70

tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat 339
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
75 80 85

ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc 387
Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
90 95 100

gga ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc 435
Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly
105 110 115

aag ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag 483
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln
120 125 130 135

cag tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc 531
Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser
140 145 150

tgc aag gct tgc ggc tac aca ttt act gac tat gaa ata cac tgg gtg	579
Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val	
155 160 165	
agg cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct	627
Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro	
170 175 180	
gaa act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata	675
Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile	
185 190 195	
gtg act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc	723
Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser	
200 205 210 215	
ctg aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag	771
Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Thr Arg Trp Phe Glu	
220 225 230	
gac tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct	819
Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser	
235 240 245	
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His His His His His	
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1 5 10 15	
gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt	96
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser	
20 25 30	
aat gga atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct	144
Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
35 40 45	
cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca	192
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro	
50 55 60	
gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	
65 70 75 80	

agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt 288
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
 85 90 95

aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 336
 Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

ggc 339
 Gly

<210> 26
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 26
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 agtc 64

<210> 27
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 27
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 aac 63

<210> 28
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 28
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 tttattttcca gcttggtc 78

<210> 29
 <211> 459
 <212> DNA
 <213> mouse

<220>

<221> CDS

<222> (19)..(459)

<220>

<221> mat_peptide

<222> (79)..(459)

<400> 29

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                   Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu
                   -20                               -15               -10

gcg gcg gcg gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct      99
Ala Ala Ala Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser
                   -5                               -1    1               5

ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag     147
Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys
                   10                               15               20

gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg agg cag     195
Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln
                   25                               30               35

aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa act     243
Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr
                   40                               45               50

ggg ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg act     291
Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr
                   60                               65               70

gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca     339
Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr
                   75                               80               85

tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg     387
Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp
                   90                               95               100

ggc caa ggg act ctg gtc act gtc tct gca gag ggt aaa tcc tca gga     435
Gly Gln Gly Thr Leu Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly
                   105                               110               115

tct ggc tcc gaa tcc aaa ccc ggg                                     459
Ser Gly Ser Glu Ser Lys Pro Gly
120                               125
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<210> 30

<211> 438

<212> DNA

<213> mouse

<220>

<221> CDS

<222> (1)..(408)

<400> 30

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gag ggt aaa tcc tca gga tct ggc tcc gaa tcc aaa ccc ggg gat gtt      48
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Pro Gly Asp Val
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1	5	10	15	
gtg atg acc cca aac cca ctc tcc ctg cct gtc agt ctt gga gat caa				96
Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln				
	20	25	30	
gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt aat gga				144
Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly				
	35	40	45	
atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca aag				192
Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys				
	50	55	60	
ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg				240
Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg				
	65	70	75	80
ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc agc aga				288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg				
	85	90	95	
gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat				336
Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His				
	100	105	110	
gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa gaa gaa				384
Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Glu Glu				
	115	120	125	
aaa ctc atc tca gaa gag gat ctg aattagtaag gggccgcctt gacctagtgc				438
Lys Leu Ile Ser Glu Glu Asp Leu				
	130	135		
<210> 31				
<211> 830				
<212> DNA				
<213> mouse				
<220>				
<221> CDS				
<222> (7)..(813)				
<220>				
<221> mat_peptide				
<222> (67)..(813)				
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Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala				
	-20	-15	-10	
gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct ggg gct gag				96
Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser Gly Ala Glu				
	-5	-1	1	5
				10
ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag gct tcg ggc				144
Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly				
	15	20	25	

tac aca ttt act gac tat gaa ata cac tgg gtg agg cag aca cct gtg	192
Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val	
30 35 40	
cat ggc ctg gaa tgg att gga gct att gat cct gaa act ggt ggt act	240
His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr	
45 50 55	
gcc tac aat cag aag ttc aag gac aag gcc ata gtg act gta gac aaa	288
Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys	
60 65 70	
tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca tct gaa gac	336
Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp	
75 80 85 90	
tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg ggc caa ggg	384
Ser Ala Val Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly	
95 100 105	
act ctg gtc act gtc tct gca gag ggt aaa tcc tca gga tct ggc tcc	432
Thr Leu Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly Ser Gly Ser	
110 115 120	
gaa tcc aaa ccc ggg gat gtt gtg atg acc cca aac cca ctc tcc ctg	480
Glu Ser Lys Pro Gly Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu	
125 130 135	
cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag	528
Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln	
140 145 150	
agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac ctg cag	576
Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln	
155 160 165 170	
aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga	624
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg	
175 180 185	
ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat	672
Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
190 195 200	
ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga gtt tat	720
Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr	
205 210 215	
ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc	768
Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr	
220 225 230	
aag ctg gaa ata aaa gaa gaa aaa ctc atc tca gaa gag gat ctg	813
Lys Leu Glu Ile Lys Glu Glu Lys Leu Ile Ser Glu Glu Asp Leu	
235 240 245	
aattagtaag cggccgc	830

<210> 32
<211> 269

<212> PRT
<213> mouse

<400> 32

Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala Ala His
-20 -15 -10 -5

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-1 1 5 10

Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly Tyr Thr
15 20 25

Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val His Gly
30 35 40

Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr Ala Tyr
45 50 55 60

Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys Ser Ser
65 70 75

Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala
80 85 90

Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly Thr Leu
95 100 105

Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser
110 115 120

Lys Pro Gly Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val
125 130 135 140

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
145 150 155

Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
160 165 170

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
175 180 185

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
190 195 200

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
205 210 215 220

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
225 230 235

Glu Ile Lys Glu Glu Lys Leu Ile Ser Glu Glu Asp Leu
240 245

<210> 33
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:c-myc tag

 <400> 33
 gaagaaaaac tcatctcaga agaggatctg 30

 <210> 34
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:p67 leader

 <400> 34
 atggtaagcg ctattgtttt atatgtgctt ttggcggcgg cggcgcattc tgcctttgcg 60

 <210> 35
 <211> 84
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 35
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 gccgtcaacg ctgcggttgt gatg 84

 <210> 36
 <211> 70
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 36
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 cagcttggtc 70

 <210> 37
 <211> 74
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 37
 ggcagcacca gcggcagcgg caagccgggc agcggcgagg gcagcaccaa gggccagggtt 60
 caactgcagc agtc 74

<210> 38
 <211> 72
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 38
 gcactagggtc aagcggccgc atgatgatga tgatgatgag aaccccgcat tgcagagaca 60
 gtgaccagag tc 72

 <210> 39
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 39
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 <210> 40
 <211> 462
 <212> DNA
 <213> mouse

 <220>
 <221> CDS
 <222> (19)..(462)

 <220>
 <221> mat_peptide
 <222> (73)...(462)

 <400> 40
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 Met Thr Ile Leu Cys Trp Leu Ala Leu Leu Ser
 -15 -10

 act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca aac cca ctc 99
 Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro Asn Pro Leu
 -5 -1 1 5

 tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct 147
 Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser
 10 15 20 25

 agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac 195
 Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr
 30 35 40

 ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc 243
 Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
 45 50 55

 aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg 291

Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly		
		60					65						70				
aca	gat	ttc	aca	ctc	aag	atc	agc	aga	gtg	gag	gct	gag	gat	ctg	gga	339	
Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly		
	75					80				85							
gtt	tat	ttc	tgc	tct	caa	agt	aca	cat	gtt	ccg	tac	acg	ttc	gga	ggg	387	
Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr	Phe	Gly	Gly		
	90				95					100					105		
ggg	acc	aag	ctg	gaa	ata	aaa	ggc	agc	acc	agc	ggc	agc	ggc	aag	ccg	435	
Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro		
				110					115					120			
ggc	agc	ggc	gag	ggc	agc	acc	aag	ggc								462	
Gly	Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly									
			125					130									
<210> 41																	
<211> 443																	
<212> DNA																	
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<222> (1)..(423)																	
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Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr		
	1			5					10					15			
aag	ggc	cat	gtt	caa	ctg	cag	cag	tct	ggg	gct	gag	ctg	gtg	agg	cct	96	
Lys	Gly	His	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro		
			20					25					30				
ggg	gct	tca	gtg	acg	ctg	tcc	tgc	aag	gct	tcg	ggc	tac	aca	ttt	act	144	
Gly	Ala	Ser	Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr		
		35				40						45					
gac	tat	gaa	ata	cac	tgg	gtg	aag	cag	aca	cct	gtg	cat	ggc	ctg	gaa	192	
Asp	Tyr	Glu	Ile	His	Trp	Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu	Glu		
	50					55					60						
tgg	att	gga	gct	att	gat	cct	gaa	act	ggt	ggt	act	gcc	tac	aat	cag	240	
Trp	Ile	Gly	Ala	Ile	Asp	Pro	Glu	Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln		
	65				70				75						80		
aag	ttc	aag	gac	aag	gcc	ata	gtg	act	gta	gac	aaa	tcc	tcc	agc	aca	288	
Lys	Phe	Lys	Asp	Lys	Ala	Ile	Val	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr		
				85					90					95			
gcc	tac	atg	gag	ctc	cgc	agc	ctg	aca	tct	gaa	gac	tct	gcc	gtc	tat	336	
Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr		
			100				105						110				
tac	tat	aca	aga	tgg	ttt	gag	gac	tgg	ggc	caa	ggg	act	ctg	gtc	act	384	
Tyr	Tyr	Thr	Arg	Trp	Phe	Glu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr		
		115				120						125					

gtc tct gca atg cgg ggt tct cat cat cat cat cat cat gcggccgctt 433
Val Ser Ala Met Arg Gly Ser His His His His His His
130 135 140

gacctagtgc 443

<210> 42
<211> 851
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (19)..(831)

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Met Thr Ile Leu Cys Trp Leu Ala Leu Leu Ser
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act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca aac cca ctc 99
Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro Asn Pro Leu
-5 -1 1 5

tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct 147
Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser
10 15 20 25

agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac 195
Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr
30 35 40

ctg cag aag cca gcc cag tct cca aag ctc ctg atc tac aaa gtt tcc 243
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
45 50 55

aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg 291
Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
60 65 70

aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga 339
Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
75 80 85

gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg 387
Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly
90 95 100 105

ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc aag ccg 435
Gly Thr Lys Leu Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro
110 115 120

ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag cag tct 483
Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln Gln Ser
125 130 135

ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag	531
Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys	
140 145 150	
gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg aag cag	579
Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Lys Gln	
155 160 165	
aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa act	627
Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr	
170 175 180 185	
ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg act	675
Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr	
190 195 200	
gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca	723
Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr	
205 210 215	
tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg	771
Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp	
220 225 230	
ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct cat cat	819
Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser His His	
235 240 245	
cat cat cat cat gcggccgctt gacctagtgc	851
His His His His	
250	
<210> 43	
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<222> (85)..(843)	
<400> 43	
aatttaaacg gatcccggtt accttctaga atg act atc ctt tgc tgg cta gcc	54
Met Thr Ile Leu Cys Trp Leu Ala	
-15	
ctt ctg tca act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca	102
Leu Leu Ser Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro	
-10 -5 -1 1 5	
aac cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct	150
Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser	
10 15 20	
tgc aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta	198

Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	
		25					30					35				
cat	tgg	tac	ctg	cag	aag	cca	ggc	cag	tct	cca	aag	ctc	ctg	atc	tac	246
His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	
	40					45				50						
aaa	gtt	tcc	aac	cga	ttt	tct	ggg	gtc	cca	gac	agg	ttc	agt	ggc	agt	294
Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	
	55				60					65					70	
gga	tca	ggg	aca	gat	ttc	aca	ctc	aag	atc	agc	aga	gtg	gag	gct	gag	342
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	
				75					80					85		
gat	ctg	gga	gtt	tat	ttc	tgc	tct	caa	agt	aca	cat	gtt	ccg	tac	acg	390
Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr	
			90					95					100			
ttc	gga	ggg	ggg	acc	aag	ctg	gaa	ata	aaa	ggc	agc	acc	agc	ggc	agc	438
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	
		105					110					115				
ggc	aag	ccg	ggc	agc	ggc	gag	ggc	agc	acc	aag	ggc	cat	gtt	caa	ctg	486
Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly	His	Val	Gln	Leu	
	120					125					130					
cag	cag	tct	ggg	gct	gag	ctg	gtg	agg	cct	ggg	gct	tca	gtg	acg	ctg	534
Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala	Ser	Val	Thr	Leu	
					140					145					150	
tcc	tgc	aag	gct	tcg	ggc	tac	aca	ttt	act	gac	tat	gaa	ata	cac	tgg	582
Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Glu	Ile	His	Trp	
				155					160					165		
gtg	aag	cag	aca	cct	gtg	cat	ggc	ctg	gaa	tgg	att	gga	gct	att	gat	630
Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Asp	
			170				175						180			
cct	gaa	act	ggt	ggt	act	gcc	tac	aat	cag	aag	ttc	aag	gac	aag	gcc	678
Pro	Glu	Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	
			185				190					195				
ata	gtg	act	gta	gac	aaa	tcc	tcc	agc	aca	gcc	tac	atg	gag	ctc	cgc	726
Ile	Val	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Arg	
	200					205					210					
agc	ctg	aca	tct	gaa	gac	tct	gcc	gtc	tat	tac	tat	aca	aga	tgg	ttt	774
Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Tyr	Thr	Arg	Trp	Phe	
	215				220					225					230	
gag	gac	tgg	ggc	caa	ggg	act	ctg	gtc	act	gtc	tct	gca	atg	cgg	ggg	822
Glu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Met	Arg	Gly	
				235				240						245		
tct	cat	cat	cat	cat	cat	cat	tagg	cgccg	ctgc	agat	tct	gatc				867
Ser	His	His	His	His	His	His										
			250													

<210> 44

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<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 44
tttaaaggcc atattggcca tgactatcct ttgctggct 39

<210> 45
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 45
tttaaaggcc atattggcca tggatgttgt gatgacccca aac 43

<210> 46
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 46
tttaaaggcc agagaggccc taatgatgat gatgatgatg agaaccccgc attg 54

<210> 47
<211> 882
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (25)..(837)

<220>
<221> mat_peptide
<222> (79)..(837)

<400> 47
ctgcagggta cggccatatt ggcc atg act atc ctt tgc tgg ctg gcc ctt 51
Met Thr Ile Leu Cys Trp Leu Ala Leu
-15 -10

ctg tca act ctg act gcc gtc aac act gcg gtt gtg atg acc cca aac 99
Leu Ser Thr Leu Thr Ala Val Asn Thr Ala Val Val Met Thr Pro Asn
-5 -1 1 5

cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc 147
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
10 15 20

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aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat	195
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His	
25 30 35	
tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa	243
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys	
40 45 50 55	
gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga	291
Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly	
60 65 70	
tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat	339
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp	
75 80 85	
ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc	387
Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe	
90 95 100	
gga ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc	435
Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly	
105 110 115	
aag ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag	483
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln	
120 125 130 135	
cag tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc	531
Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser	
140 145 150	
tgc aag gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg	579
Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val	
155 160 165	
agg cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct	627
Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro	
170 175 180	
gaa act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata	675
Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile	
185 190 195	
gtg act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc	723
Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser	
200 205 210 215	
ctg aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag	771
Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Thr Arg Trp Phe Glu	
220 225 230	
gac tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct	819
Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser	
235 240 245	
cat cat cat cat cat tagggcctct ctggccgac cccgaattt	867
His His His His His	
250	
ccccgatcgt tcaaa	882

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<220>  
<221> CDS  
<222> (25) .. (786)
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ctgcagggta	cggccatatt	ggcc	atg	gat	gtt	gtg	atg	acc	cca	aac	cca					51
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			1					5								
ctc	tcc	ctg	cct	gtc	agt	ctt	gga	gat	caa	gcc	tcc	atc	tct	tgc	aga	99
Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	
10					15					20					25	
tct	agt	cag	agc	ctt	tta	cac	agt	aat	gga	atc	acc	tat	tta	cat	tgg	147
Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	His	Trp	
				30					35					40		
tac	ctg	cag	aag	cca	ggc	cag	tct	cca	aag	ctc	ctg	atc	tac	aaa	gtt	195
Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	
			45					50					55			
tcc	aac	cga	ttt	tct	ggg	gtc	cca	gac	agg	ttc	agt	ggc	agt	gga	tca	243
Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	
		60					65					70				
ggg	aca	gat	ttc	aca	ctc	aag	atc	agc	aga	gtg	gag	gct	gag	gat	ctg	291
Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	
	75					80					85					
gga	gtt	tat	ttc	tgc	tct	caa	agt	aca	cat	gtt	cgc	tac	acg	ttc	gga	339
Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr	Phe	Gly	
	90				95					100					105	
ggg	ggg	acc	aag	ctg	gaa	ata	aaa	ggc	agc	acc	agc	ggc	agc	ggc	aag	387
Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	
				110				115						120		
ccg	ggc	agc	ggc	gag	ggc	agc	acc	aag	ggc	cat	gtt	caa	ctg	cag	cag	435
Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly	His	Val	Gln	Leu	Gln	Gln	
			125					130					135			
tct	ggg	gct	gag	ctg	gtg	agg	cct	ggg	gct	tca	gtg	acg	ctg	tcc	tgc	483
Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala	Ser	Val	Thr	Leu	Ser	Cys	
		140					145					150				
aag	gct	tcg	ggc	tac	aca	ttt	act	gac	tat	gaa	ata	cac	tgg	gtg	agg	531
Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Glu	Ile	His	Trp	Val	Arg	
	155					160					165					
cag	aca	cct	gtg	cat	ggc	ctg	gaa	tgg	att	gga	gct	att	gat	cct	gaa	579
Gln	Thr	Pro	Val	His	Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Asp	Pro	Glu	
170					175					180					185	
act	ggt	ggt	act	gcc	tac	aat	cag	aaq	ttc	aag	gac	aag	gcc	ata	gtg	627

Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Ile	Val		
				190					195					200			
act	gta	gac	aaa	tcc	tcc	agc	aca	gcc	tac	atg	gag	ctc	cgc	agc	ctg	675	
Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu		
			205					210					215				
aca	tct	gaa	gac	tct	gcc	gtc	tat	tac	tat	aca	aga	tgg	ttt	gag	gac	723	
Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Tyr	Thr	Arg	Trp	Phe	Glu	Asp		
		220					225					230					
tgg	ggc	caa	ggg	act	ctg	gtc	act	gtc	tct	gca	atg	cgg	ggg	tct	cat	771	
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Met	Arg	Gly	Ser	His		
	235					240					245						
cat	cat	cat	cat	cat	tagggcctct	ctggccgatc	ccccgaattt	ccccgatcgt	826								
His	His	His	His	His													
					250												
tcaaacattt	ggcaataaag															846	

<210> 49
 <211> 738
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (19)..(687)
 <223> mature peptide is coded by nucleotides 49 to 687

<400> 49																	
cccgggtacc	cttctaga	ctc	gtg	aca	ggt	ggt	gat	ggg	gcc	caa	tcc	cag	51				
		Leu	Val	Thr	Val	Val	Asp	Gly	Ala	Gln	Ser	Gln					
		1				5					10						
ggt	caa	ctg	cag	cag	tct	ggg	gct	gag	ctg	gtg	agg	cct	ggg	gct	tca	99	
Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala	Ser		
		15				20					25						
gtg	acg	ctg	tcc	tgc	aag	gct	tcg	ggc	tac	aca	ttt	act	gac	tat	gaa	147	
Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Glu		
		30				35					40						
ata	cac	tgg	gtg	agg	cag	aca	cct	gtg	cat	ggc	ctg	gaa	tgg	att	gga	195	
Ile	His	Trp	Val	Arg	Gln	Thr	Pro	Val	His	Gly	Leu	Glu	Trp	Ile	Gly		
	45					50					55						
gct	att	gat	cct	gaa	act	ggg	ggg	act	gcc	tac	aat	cag	aag	ttc	aag	243	
Ala	Ile	Asp	Pro	Glu	Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe	Lys		
	60				65				70						75		
gac	aag	gcc	ata	gtg	act	gta	gac	aaa	tcc	tcc	agc	aca	gcc	tac	atg	291	
Asp	Lys	Ala	Ile	Val	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met		
			80						85					90			
gag	ctc	cgc	agc	ctg	aca	tct	gaa	gac	tct	gcc	gtc	tat	tac	tat	aca	339	
Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Tyr	Thr		
			95					100					105				

aga tgg ttt gag gac tgg ggc caa ggg act ctg gtc act gtc tct gca	387
Arg Trp Phe Glu Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala	
110 115 120	
gcc aaa aca aca ccc cca tca gtc tat cca ctg gcc cct ggg tgt gga	435
Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Cys Gly	
125 130 135	
gat aca act ggt tcc tct gtg act ctg gga tgc ctg gtc aag ggc tac	483
Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr	
140 145 150 155	
ttc cct gag tca gtg act gtg act tgg aac tct gga tcc ctg tcc agc	531
Phe Pro Glu Ser Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser	
160 165 170	
agt gtg cac acc ttc cca gct ctc ctg cag tct gga ctc tac act atg	579
Ser Val His Thr Phe Pro Ala Leu Leu Gln Ser Gly Leu Tyr Thr Met	
175 180 185	
agc agc tca gtg act gtc ccc tcc agc acc tgg cca agt cag acc gtc	627
Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Gln Thr Val	
190 195 200	
acc tgc agc gtt gct cac cca gcc agc agc acc acg gtg gac aaa aaa	675
Thr Cys Ser Val Ala His Pro Ala Ser Ser Thr Thr Val Asp Lys Lys	
205 210 215	
ctt gag ccc agc gcggccgctg caggtcttga tcctttcctg ggacccggca	727
Leu Glu Pro Ser	
220	
agaaccaaaa a	738
<210> 50	
<211> 42	
<212> DNA	
<213> mouse	
<400> 50	
gcactaggtc aagcggccgc ttactaacac tcattcctgt tg	42
<210> 51	
<211> 753	
<212> DNA	
<213> mouse	
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<221> CDS	
<222> (7)..(705)	
<220>	
<221> mat_peptide	
<222> (67)..(705)	
<400> 51	
tctaga atg gta agc gct att gtt tta tat gtg ctt ttg gcg gcg gcg	48
Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala	
-20 -15 -10	

gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct ggg gct gag	96
Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser Gly Ala Glu	
-5 -1 1 5 10	
ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag gct tgc ggc	144
Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly	
15 20 25	
tac aca ttt act gac tat gaa ata cac tgg gtg agg cag aca cct gtg	192
Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val	
30 35 40	
cat ggc ctg gaa tgg att gga gct att gat cct gaa act ggt ggt act	240
His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr	
45 50 55	
gcc tac aat cag aag ttc aag gac aag gcc ata gtg act gta gac aaa	288
Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys	
60 65 70	
tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca tct gaa gac	336
Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp	
75 80 85 90	
tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg ggc caa ggg	384
Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly	
95 100 105	
act ctg gtc act gtc tct gca gcc aaa aca aca ccc cca tca gtc tat	432
Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr	
110 115 120	
cca ctg gcc cct ggg tgt gga gat aca act ggt tcc tct gtg act ctg	480
Pro Leu Ala Pro Gly Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu	
125 130 135	
gga tgc ctg gtc aag ggc tac ttc cct gag tca gtg act gtg act tgg	528
Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Ser Val Thr Val Thr Trp	
140 145 150	
aac tct gga tcc ctg tcc agc agt gtg cac acc ttc cca gct ctc ctg	576
Asn Ser Gly Ser Leu Ser Ser Ser Val His Thr Phe Pro Ala Leu Leu	
155 160 165 170	
cag tct gga ctc tac act atg agc agc tca gtg act gtc ccc tcc agc	624
Gln Ser Gly Leu Tyr Thr Met Ser Ser Ser Val Thr Val Pro Ser Ser	
175 180 185	
acc tgg acc tgc agc gtt gct cac cca gcc agc agc cca agt cag acc	672
Thr Trp Thr Cys Ser Val Ala His Pro Ala Ser Ser Pro Ser Gln Thr	
190 195 200	
gtc acc acg gtg gac aaa aaa ctt gag ccc agc tagtaatgag cggccgctgc	725
Val Thr Thr Val Asp Lys Lys Leu Glu Pro Ser	
205 210	
agatctgac ctttctggg acccgga	753

<210> 52

<211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:nt 2253 to 2271
 of pDAB439

 <400> 52
 tgcacgtgtt ctccttttt 19

 <210> 53
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:nt 4256 to 4308
 of pDAB439

 <400> 53
 ggtacggcca tattggccga gctcggcctc tctggccgat cccc 44

 <210> 54
 <211> 63
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:nt 4744 to 4807
 of pDAB439

 <400> 54
 gcggccgctt taacgcccgg gcatttaaatt ggcgcgccgc gatcgcttgc agatctgcat 60
 ggg 63

 <210> 55
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:nt 5417 to 5436
 of pDAB439

 <400> 55
 ggggactcta gaggatccag 20

 <210> 56
 <211> 24
 <212> PRT
 <213> Zea mays

 <400> 56
 Pro Gly Ser Pro Ala Pro Ala Ala Pro Lys Asn Gly Leu Gly Glu Arg
 1 5 10 15

Pro Glu Ser Leu Asp Val Arg Gly
20